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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:02

Input Set : N:\Crf3\RULE60\10788992.raw.txt
 Output Set: N:\CRF4\09172004\J788992.raw

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
 - 5 (i) APPLICANT: Gilula, Norton B
Cravatt, Benjamin F
Lerner, Richard A
 - 9 (ii) TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
 - 11 (iii) NUMBER OF SEQUENCES: 54
 - 13 (iv) CORRESPONDENCE ADDRESS:
 - 14 (A) ADDRESSEE: The Scripps Research Institute
 - 15 (B) STREET: 10550 North Torrey Pines Road
 - 16 (C) CITY: La Jolla
 - 17 (D) STATE: California
 - 18 (E) COUNTRY: US
 - 19 (F) ZIP: 92037
 - 21 (v) COMPUTER READABLE FORM:
 - 22 (A) MEDIUM TYPE: Floppy disk
 - 23 (B) COMPUTER: IBM PC compatible
 - 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - 27 (vi) CURRENT APPLICATION DATA:
 - C--> 28 (A) APPLICATION NUMBER: US/10/788,992
 - C--> 29 (B) FILING DATE: 26-Feb-2004
 - 30 (C) CLASSIFICATION: 435
 - 32 (vii) PRIOR APPLICATION DATA:
 - W--> 33 (A) APPLICATION NUMBER: US/08/743,168
 - 34 (B) FILING DATE: 01-May-1998
 - W--> 35 (A) APPLICATION NUMBER: US 08/489,535
 - 36 (B) FILING DATE: 12-JUN-1995
 - 38 (viii) ATTORNEY/AGENT INFORMATION:
 - 39 (A) NAME: Fitting, Thomas
 - 40 (B) REGISTRATION NUMBER: 34,163
 - 41 (C) REFERENCE/DOCKET NUMBER: TSRI 485.2
 - 43 (ix) TELECOMMUNICATION INFORMATION:
 - 44 (A) TELEPHONE: (619) 784-2937
 - 45 (B) TELEFAX: (619) 784-9399
- 48 (2) INFORMATION FOR SEQ ID NO: 1:
 - 50 (i) SEQUENCE CHARACTERISTICS:
 - 51 (A) LENGTH: 783 base pairs
 - 52 (B) TYPE: nucleic acid
 - 53 (C) STRANDEDNESS: double
 - 54 (D) TOPOLOGY: linear
 - 56 (ii) MOLECULE TYPE: cDNA
 - 58 (iii) HYPOTHETICAL: NO

ENTERED

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60 (iv) ANTI-SENSE: NO
 63 (ix) FEATURE:
 64 (A) NAME/KEY: CDS
 65 (B) LOCATION: 1..783
 68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 70 AGC CCA GGA GGT TCC TCA GGG GGT GAG GGG GCT CTC ATT GGA TCT GGA 48
 71 Ser Pro Gly Gly Ser Ser Gly Gly Glu Ala Leu Ile Gly Ser Gly
 72 1 5 10 15
 74 GGT TCC CCT CTG GGT TTA GGC ACT GAC ATT GGC GGC AGC ATC CGG TTC 96
 75 Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe
 76 20 25 30
 78 CCT TCT GCC TTC TGC GGC ATC TGT GGC CTC AAG CCT ACT GGC AAC CGC 144
 79 Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly Asn Arg
 80 35 40 45
 82 CTC AGC AAG AGT GGC CTG AAG GGC TGT GTC TAT GGA CAG ACG GCA GTG 192
 83 Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val
 84 50 55 60
 86 CAG CTT TCT CTT GGC CCC ATG GCC CGG GAT GTG GAG AGC CTG GCG CTA 240
 87 Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu Ala Leu
 88 65 70 75 80
 90 TGC CTG AAA GCT CTA CTG TGT GAG CAC TTG TTC ACC TTG GAC CCT ACC 288
 91 Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp Pro Thr
 92 85 90 95
 94 GTG CCT CCC TTT CCC TTC AGA GAG GAG GTC TAT AGA AGT TCT AGA CCC 336
 95 Val Pro Pro Phe Pro Arg Glu Glu Val Tyr Arg Ser Ser Arg Pro
 96 100 105 110
 98 CTG CGT GTG GGG TAC TAT GAG ACT GAC AAC TAT ACC ATG CCC AGC CCA 384
 99 Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro Ser Pro
 100 115 120 125
 102 GCT ATG AGG AGG GCT CTG ATA GAG ACC AAG CAG AGA CTT GAG GCT GCT 432
 103 Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu Ala Ala
 104 130 135 140
 106 GGC CAC ACG CTG ATT CCC TTC TTA CCC AAC AAC ATA CCC TAC GCC CTG 480
 107 Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr Ala Leu
 108 145 150 155 160
 110 GAG GTC CTG TCT GCG GGC GGC CTG TTC AGT GAC GGT GGC CGC AGT TTT 528
 111 Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg Ser Phe
 112 165 170 175
 114 CTC CAA AAC TTC AAA GGT GAC TTT GTG GAT CCC TGC TTG GGA GAC CTG 576
 115 Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly Asp Leu
 116 180 185 190
 118 ATC TTA ATT CTG AGG CTG CCC AGC TGG TTT AAA AGA CTG CTG AGC CTC 624
 119 Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu Ser Leu
 120 195 200 205
 122 CTG CTG AAG CCT CTG TTT CCT CGG CTG GCA GCC TTT CTC AAC AGT ATG 672
 123 Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn Ser Met
 124 210 215 220
 126 CGT CCT CGG TCA GCT GAA AAG CTG TGG AAA CTG CAG CAT GAG ATT GAG 720
 127 Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu Ile Glu

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128	225	230	235	240	
130	ATG TAT CGC CAG TCT GTG ATT GCC CAG TGG AAA GCG ATG AAC TTG GAT				768
131	Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu Asp				
132	245	250	255		
134	GTG CTG CTG ACC TAA				783
135	Val Leu Leu Thr				
136	260				
139	(2) INFORMATION FOR SEQ ID NO: 2:				
141	(i) SEQUENCE CHARACTERISTICS:				
142	(A) LENGTH: 260 amino acids				
143	(B) TYPE: amino acid				
144	(D) TOPOLOGY: linear				
146	(ii) MOLECULE TYPE: protein				
148	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:				
150	Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly				
151	1	5	10	15	
153	Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe				
154	20	25	30		
156	Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly Asn Arg				
157	35	40	45		
159	Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val				
160	50	55	60		
162	Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu Ala Leu				
163	65	70	75	80	
165	Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp Pro Thr				
166	85	90	95		
168	Val Pro Pro Phe Pro Phe Arg Glu Glu Val Tyr Arg Ser Ser Arg Pro				
169	100	105	110		
171	Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro Ser Pro				
172	115	120	125		
174	Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu Ala Ala				
175	130	135	140		
177	Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr Ala Leu				
178	145	150	155	160	
180	Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg Ser Phe				
181	165	170	175		
183	Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly Asp Leu				
184	180	185	190		
186	Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu Ser Leu				
187	195	200	205		
189	Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn Ser Met				
190	210	215	220		
192	Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu Ile Glu				
193	225	230	235	240	
195	Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu Asp				
196	245	250	255		
198	Val Leu Leu Thr				
199	260				
202	(2) INFORMATION FOR SEQ ID NO: 3:				

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PATENT APPLICATION: US/10/788,992 **TIME:** 08:55:02

Input Set : N:\Crf3\RULE60\10788992.raw.txt
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204 (i) SEQUENCE CHARACTERISTICS:
205 (A) LENGTH: 22 base pairs
206 (B) TYPE: nucleic acid
207 (C) STRANDEDNESS: single
208 (D) TOPOLOGY: linear
210 (ii) MOLECULE TYPE: cDNA
212 (iii) HYPOTHETICAL: NO
214 (iv) ANTI-SENSE: NO
218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
220 CGGAATTCGG NGGNNGARGGN GC
222 (2) INFORMATION FOR SEQ ID NO: 4:
224 (i) SEQUENCE CHARACTERISTICS:
225 (A) LENGTH: 5 amino acids
226 (B) TYPE: amino acid
227 (D) TOPOLOGY: linear
229 (ii) MOLECULE TYPE: peptide
231 (v) FRAGMENT TYPE: internal
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
237 Gly Gly Glu Gly Ala
238 1 5
240 (2) INFORMATION FOR SEQ ID NO: 5:
242 (i) SEQUENCE CHARACTERISTICS:
243 (A) LENGTH: 31 amino acids
244 (B) TYPE: amino acid
245 (D) TOPOLOGY: linear
247 (ii) MOLECULE TYPE: peptide
249 (v) FRAGMENT TYPE: internal
253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
255 Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly Ser
256 1 5 10 15
258 Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe Pro
259 20 25 30
261 (2) INFORMATION FOR SEQ ID NO: 6:
263 (i) SEQUENCE CHARACTERISTICS:
264 (A) LENGTH: 15 amino acids
265 (B) TYPE: amino acid
266 (D) TOPOLOGY: linear
268 (ii) MOLECULE TYPE: peptide
270 (v) FRAGMENT TYPE: internal
274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
276 Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser
277 1 5 10 15
279 (2) INFORMATION FOR SEQ ID NO: 7:
281 (i) SEQUENCE CHARACTERISTICS:
282 (A) LENGTH: 15 amino acids
283 (B) TYPE: amino acid
284 (D) TOPOLOGY: linear
286 (ii) MOLECULE TYPE: peptide
288 (v) FRAGMENT TYPE: internal

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Input Set : N:\Crf3\RULE60\10788992.raw.txt
Output Set: N:\CRF4\09172004\J788992.raw

292 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
294 Ala Leu Ile Gly Ser Gly Ser Pro Leu Gly Leu Gly Thr Asp
295 1 5 10 15
297 (2) INFORMATION FOR SEQ ID NO: 8:
299 (i) SEQUENCE CHARACTERISTICS:
300 (A) LENGTH: 15 amino acids
301 (B) TYPE: amino acid
302 (D) TOPOLOGY: linear
304 (ii) MOLECULE TYPE: peptide
306 (v) FRAGMENT TYPE: internal
310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
312 Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe Pro Ser Ala
313 1 5 10 15
315 (2) INFORMATION FOR SEQ ID NO: 9:
317 (i) SEQUENCE CHARACTERISTICS:
318 (A) LENGTH: 15 amino acids
319 (B) TYPE: amino acid
320 (D) TOPOLOGY: linear
322 (ii) MOLECULE TYPE: peptide
324 (v) FRAGMENT TYPE: internal
328 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
330 Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr
331 1 5 10 15
333 (2) INFORMATION FOR SEQ ID NO: 10:
335 (i) SEQUENCE CHARACTERISTICS:
336 (A) LENGTH: 15 amino acids
337 (B) TYPE: amino acid
338 (D) TOPOLOGY: linear
340 (ii) MOLECULE TYPE: peptide
342 (v) FRAGMENT TYPE: internal
346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
348 Gly Leu Lys Pro Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys
349 1 5 10 15
351 (2) INFORMATION FOR SEQ ID NO: 11:
353 (i) SEQUENCE CHARACTERISTICS:
354 (A) LENGTH: 15 amino acids
355 (B) TYPE: amino acid
356 (D) TOPOLOGY: linear
358 (ii) MOLECULE TYPE: peptide
360 (v) FRAGMENT TYPE: internal
364 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
366 Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val Gln
367 1 5 10 15
369 (2) INFORMATION FOR SEQ ID NO: 12:
371 (i) SEQUENCE CHARACTERISTICS:
372 (A) LENGTH: 15 amino acids
373 (B) TYPE: amino acid
374 (D) TOPOLOGY: linear
376 (ii) MOLECULE TYPE: peptide

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/17/2004
PATENT APPLICATION: US/10/788,992 TIME: 08:55:03

Input Set : N:\Crf3\RULE60\10788992.raw.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 11,14,20
Seq#:33; N Pos. 14
Seq#:38; Xaa Pos.5
Seq#:54; N Pos. 780,786,789,792,795,798,804,810,813,816,819

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:03

Input Set : N:\Crf3\RULE60\10788992.raw.txt
Output Set: N:\CRF4\09172004\J788992.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:957 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:35
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0